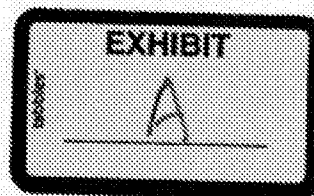


GAP of: NvEcR10prtseqwhole.txt check: 4332 from: 1 to: 444

to: MpEcR check: 9113 from: 1 to: 450



Symbol comparison table:  
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430  
BLOSUM62 amino acid substitution matrix.  
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl.  
Acad.

Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1518	Length:	474
Ratio:	3.419	Gaps:	6
Percent Similarity:	79.762	Percent Identity:	72.857

*N. viridula* EcR (1)  
vs *M. persicae* EcR

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

GAP of: NvEcR11prtseqwhole.txt check: 6564 from: 1 to: 464

to: MpEcR check: 9113 from: 1 to: 450

Symbol comparison table:  
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430  
BLOSUM62 amino acid substitution matrix.  
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl.  
Acad.

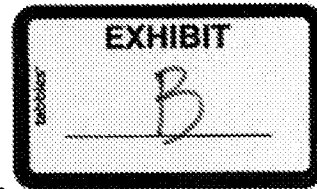
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1510	Length:	496
Ratio:	3.356	Gaps:	7
Percent Similarity:	80.144	Percent Identity:	73.445

*N. viridula* (2)  
vs *M. persicae* EcR

GAP of: MpEcR check: 9113 from: 1 to: 450

to: BtEcR check: 8626 from: 1 to: 416



Symbol comparison table:  
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430  
BLOSUM62 amino acid substitution matrix.  
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl.  
Acad.  
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1450	Length:	451
Ratio:	3.486	Gaps:	6
Percent Similarity:	78.554	Percent Identity:	71.566

M pusillae Eck  
vs B tabaci Eck